

09757982-012902

TCGACCCACGCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCGCCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCGCAGGGTGGGTGCCCCGCGCTGCAGCGTCCGCCGGGGCGGCGGGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCGGCCCAGCGGCTTTCCGACGGCGGCGCCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAAAACTCCCAACTTCTGAGTTCTAAAGTTCTGTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCTCAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTTTGAATAGAAAAGAAAATTGGTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCAATTGAAGATAATGAACTAAACATAGTTTTTGAAGTACGAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGAAGTATTTTGT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTCATT
ACAGCCACTG
GGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCAC
ATTCCTTAGTTGGTACGCCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCCTCAGATCACTATTCAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCATTATGTCTGGGTGTTAAGATTAATATTTAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTCATATAAGCTTCATTTTGTACCAGTACCTAAATCACCTCCTTGC
AACCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTCTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCTTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAACTATTTGAGA
AACATTTAGAAGCTTAGCTTATACATTCAAATGTAAGTATTAAATGTGAAGATTTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTAATATTTTTGATATTCTCTTGCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTTATTTGTTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
TATATTTCAA

Fig. 1

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TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
CATAAGTTTT
ATTGAAGTTCTGATCGGTCCCCCTTCAGAAATTTTTTTATATTCTTCAAGTTACTTTCTTA
TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
GATATTTGGT
ATACCAATACTTTTCTGGATTGAAAACTTTTTTTTAAACTTTTTTAAAAATTTGGGCCACTCTGTATGCA
TATGTTTGGT
CTTGTTAAAGAGGAAGAAAGGATGTGTGTTTACTGTACCTGTGAATGTTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTTCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTTTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
TGCTTTTCGTATTAGTGGCGACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCAC
GTTAAAGGAC
TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAAGTCTGCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
GCATTTGTAAACTTAAAAAANWAWAAAGGCCAAAAAGTCTGAACCTTGTTTTCTGAAATCTAATC
AGTTATGTAT
GGTTTTCTGAAGGTAATTTTATTTTGGAAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTCTCTGAG
GGCTAGATGC
ATTTTTTTTCTCACACTCTTAATGACTTTTAAACATTTTACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATCTTATTGACCATTAATGTCATGTTTCATTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTTTAAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAATTCATTATTTCTATATGTGGAACTTTTGGCT
TCGAATATTG
TATCTTTTTTAAATCTAAATGTTTCATATTTTCTCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
TTGAATGGAA
TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTTCATAAGTAAATTTTATATTGATTAAGTTAACTTTTGAATTGATTTGAGGAGCAG
TAAAATGAAA
GCTATATCTATTNCTAAACCTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
TTGTTTTGTA
TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAAATAAAGTGCTCAACAATGTG
CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTTCATGAATGCTTTACCATTCAACATAGTATCT
ATTACAAAAC
ACCTTTCTTGTATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAA
ATGTTACTCA
CATTAAATGTTTATTCTTTTAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTTGTGAAATACTTTTATTTTGTATGC
TTTAAATATA
CATACAAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
AATAAAAAATG
AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG

Fig. 1 (continued)

MDEQSQGMQGPVPQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVVVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVKGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKKIEQCDYPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

Fig. 1 (continued)

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GTCGACCCACGCGTCCGGTGGAGTATAATACTTTGTCATTATGAGATGTCGTCTCTCGG
TGCCCTCCTTTGTGCAAAATTAAATTTGATGACTTGCAGTTTTTTGAAAAC TGCGGTGGAGG
AAGTTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTACAGAAATATGC
TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCATAACAACACATGTC
CTTGGTTGGAACTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGAGA
AACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAaaaaaacgagagatt
AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTGGGAAGC
TGATGCCAAGAAACGGCCATCATTTCAAGCAAATCATTTCATCCTGGAGTCCATGTCAAA
TGACACGAGCCTTCTGACAAGTGTAACTCATTCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTTTCCTCTTGTCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTATGTGATGCAGATCACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTTCAGTGATTTTGACTTGTGAGAAGGTGACGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACCTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTtagGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTATTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAAATGAATACTTTTTAGTTTG
TATTTGACTTTATTTCTTTATTCAAATCATTTTTTAAAACTTACATTTTGAACAAACAC
TCTTAACCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCCTGCACTCTAGCCTGGGCAAGAGAACAAGATCCTGTCTCAAAAAACAAA
AAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWI SQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDM
HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTHMS
LVGTFPWWAPEVIQSLPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAWLVEKNERL
TIPSSCPRSFAELLHQWEADAKRPSFKQII SILESMSNDTSLPDKCNSFLHNKAEWRC
EIEATLERLKLRLDL SFKEQELKERERRLKMWEQKLTEQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSQMQINMQ
AKQNSSKTTSKRRGKKVNMLGFSDFDLSEGD DDDDDDDGEEEDNDMDNSE

Fig. 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
GACAGGCGCTGGGCGCGGCGCTGCAGCTGGGTTCGAGCGCTGCTGCTGCGCTTCACGGGCA
AGCCCCGGCGGGCCTACGGCTTGGGGCGGCGGGCCCCGGCGGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTTC
CTAACCGTCTCCGCTTCTTCCGCCAGTGGTGGCGGGGCTGGCGGCGCGGTTCAGCGGC
AGTTCGTGGTGGCGGCTGGGGCTGCGCGGGGCCCTTGGCGGCGGGCAGTCTTCTGGCCT
TCGGGCTAGGGCTGGGCTCATCGAGGAAAAACAGGCGGAGAGCGGGCGGGCGGTCTCGG
CCTGTCAGGAGATCCAGGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGCAGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCAGTGTCTGTGTATGAAGCCACCATGCCCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCAGGGTTCCTTCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGGCCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTCTTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCCAAGCAACTAGCCCCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTT
CCGTGCGCGCTGCTGCCAGGGGCCCTGGTCCGACTACCCTGATGTGCTGCCCTCACGCCTCC
ACCCTGAAGGCCTGGGCCATGGCCGGACGCTGTTCCCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGC
TGCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAG
ATTTTGGCTGCTGCCCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCCGTCTTG
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGCTACCTGCCTGCCCCAGTCACTGCCCTCCAGACGTGAGAC
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTTGTGTGGAAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCTAGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCGTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAAGTGAAGTTCAGTCTGCAGTCCCTCTGC
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCACTGCCAGAG
TTTGGCTGTGACCTTTGCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCACGTTCACTTACGGG
AGTGGGAAATTACATGAGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
TAAATGCAATTTACAACCTGCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCC

Fig. 3

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Met Ala
Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
5 10 15
Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
20 25 30
Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35 40 45 50
Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
55 60 65
Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
70 75 80
Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
85 90 95
Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
100 105 110
Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115 120 125 130
Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
135 140 145
Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
150 155 160
Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
165 170 175
Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180 185 190
Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195 200 205 210
Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
215 220 225

Fig. 3 (continued)

Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	Leu	Val	
			230					235						240		
Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	Thr	Tyr	
		245					250					255				
Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	Asn	Ile	
	260					265					270					
Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	Pro	Gly	
275					280					285					290	
Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	Pro	Glu	
				295					300					305		
Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	Tyr	Pro	
			310					315						320		
Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	Arg	Leu	
		325					330						335			
Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	Leu	Val	
		340				345						350				
Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	
355					360					365					370	
Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	Phe	Gly	
				375					380					385		
Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	Ser	Ser	
			390					395					400			
Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	Glu	Val	
		405					410					415				
Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	Lys	Ala	
		420				425					430					

Fig. 3 (continued)

Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
 435 440 445 450
 Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
 455 460 465
 Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
 470 475 480
 Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
 485 490 495
 Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
 500 505 510
 His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
 515 520 525 530
 Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
 535 540 545
 Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
 550 555 560
 Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
 565 570 575
 Ala Ala Leu

Fig. 3 (continued)

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GTCGACCCACGCGGTCCGCCCACGCGTTCGGAGACATGTCTCTGTGTTTCTCTCCCTCCGCTTTTGAGTCCGTTGAAGACACAATTTCTCTCTGTGCGGTGCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAGGCTGCTGGTTGGCTGCCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTCAGCTCCCTGCAGCAGTCATGGGGCAGGGTCCCCGAGTCCGTAATCCCCATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCGTACTCAGCTTAAGTGGAGCATCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGCAAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGACGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC CGGAAACGGCTCACAAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCCGGTGGACAACCAGCAAGCCATGGTGCGCAGGGAGTCTGTGGTCAATCTGGAGAAGTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCCTTCAGCATCGTGTCCCTGTGCAACCACCTCACCCGCTCGCTGATGAAGAAGGTGCACTTGAGGCCGGATGAGGACCTGAGGAAGTGTGAGAGTGACACTGAGGAGGACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCTCCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGGGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGCGTCTGAGCACTTTGCAAGAGAGATGGGCCCCAAGGAATTCAGAAGAGCTTGCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAGGCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCCTCTGTCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA TAAAGGACATCCTCATCATCACGGGGTGAAGGTCAGACTAAGGCAGCCTTCTTCACAGGCTGAGGGGGTTCAGAACCAGCCTGGCCAAAAATTACACCAGAGAGACAGAGTCCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACCTTGGGTGTGAGGGACCAATCCTGTGACCTCCAGAACCATGGAAGCCAGGACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGCCGCCATGTTGTAATTTTGCTCATTTTTATTAACTTCTGGTTTACCTGATGCTTGCTTCTTTTAGGGCTACCCCCATCTCATTTCTTTAGCCCCGTGTGCTGTAACTCTGAGGGGGGGCACCCAGTGGGGTGCTGAGTGGGCAGAATCTCA GAAGGTCCTCCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTCCTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGACTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGGCAGGGGAATTGCTTGAAGTCAAGGAGTGGAGACCAGCCTGGGCAACATGGCAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGTAGGCACCTGGCATCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTTAAGCCCAGAAGGTGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACCTCAGTCTGGGTGACAGAGAGACCATATCCAAAAAAGGGCGGCCGC

LFDSL SVVLSLSGAS PFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKVHLRPDEDLRNCESDTEEDIARRKALHPRRRSSTS

Fig. 4

T A L A K E L R E L R I E E T N R P M	19
G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG	57
K K V T D Y S S S S E E S S E E E E	39
AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG	117
E D G E S E T H D G T V A V S D I P R L	59
GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG	177
I P T G A P G S N E Q Y N V G M V G T H	79
ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG ACG CAT	237
G L E T S H A D S F S G S I S R E G T L	99
GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG	297
M I R E T S G E K K R S G H S D S N G F	119
ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT	357
A G H I N L P D L V Q Q S H S P A G T P	139
GCT GGC CAC ATC AAC CTC CCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG	417
T E G L G R V S T H S Q E M D S G T E Y	159
ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT	477
G M G S S T K A S F T P F V D P R V Y Q	179
GGC ATG GGG AGC AGC ACC AAA GCC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG	537
T S P T D E D E E D E E S S A A A L F T	199
ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GCC GCA GCT CTG TTT ACT	597
S E L L R Q E Q A K L N E A R K I S V V	219
AGC GAA CTT CTT AGG CAA GAA CAG GCC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA	657
N V N P T N I R P H S D T P E I R K Y K	239
AAT GTA AAC CCA ACC AAC ATT CGG CCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG	717
K R F N S E I L C A A L W G V N L L V G	259
AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG	777
T E N G L M L L D R S G Q G K V Y N L I	279
ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC	837
N R R R F Q Q M D V L E G L N V L V T I	299
AAC CGG AGG GGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT	897
S G K K N K L R V Y Y L S W L R N R I L	319
TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA	957
H N D P E V E K K Q G W I T V G D L E G	339
CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC	1017

Fig. 5

C I H Y K V V K Y E R I K F L V I A L K 359
 TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG 1077

 N A V E I Y A W A P K P Y H K F M A F K 379
 AAT GCT GTG GAA ATA TAT GCT TGG GCT CCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG 1137

 S F A D L Q H K P L L V D L T V E E G Q 399
 TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA 1197

 R L K V I F G S H T G F H V I D V D S G 419
 AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA 1257

 N S Y D I Y I P S H I Q G N I T P H A I 439
 AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT CCT CAT GCT ATT 1317

 V I L P K 444
 GTC ATC TTG CCT AAA 1332

Fig. 5 (continued)

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